



SEQUENCE LISTING

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<120> RECOMBINANT VACCINE AGAINST BOTULINUM
NEUROTOXIN

<130> A33626-A 067252.0107

<140> 09/910,186
<141> 2001-07-20

<150> 09/611,419
<151> 2000-07-06

<150> PCT/US00/12890
<151> 2000-05-12

<150> 60/133,865
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<150> 60/133,866
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<150> 60/146,192
<151> 1999-07-29

<150> 08/123,975
<151> 1993-09-21

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<170> FastSEQ for Windows Version 4.0

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<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<400> 1

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tccaaaatca acatcggttc taaaagttAAC ttgcgtccga tcgacaagaa tcagatccag 180
ctgttcaatc tggaatcttc caaaatcgaa gttatcctga agaatgctat cgtatacaac 240
tctatgtacg aaaacttctc cacctccttc tggatccgta tcccgaaata cttcaactcc 300
atctctctga acaatgaata caccatcatc aactgcattgg aaaacaattc tggttggaaa 360
gtatctctga actacggtga aatcatctgg actctgcagg acactcagga aatcaaacag 420
cgtgttgtat tcaaatactc tcagatgatc aacatctctg actacatcaa tcgctggatc 480
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atcgaccaga aaccgatctc caatctgggt aacatccacg cttctaataa catcatgttc 600
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gacaaagaac tgaacgaaaa agaaatcaaa gacctgtacg acaaccagtc caattctgg 720
atctctgaaag acttctgggg tgactacctg cagtgacaca aaccgtacta catgtgaat 780
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ctgaaaggtc cgcgtgggtc tggatgtact accaacatct acctgaactc ttccctgtac 900
cgtgttacca aattcatcat caagaaatac gcgtctggta acaaggacaa tatcgttcgc 960
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aatgcttctc aggctgggtg agaaaagatc ttgtctgctc tggaaatccc ggacggttgg 1080
aatctgtctc aggtagttgt aatgaaatcc aagaacgacc agggatcac taacaaatgc 1140
aaaatgaatc tgcaggacaa caatggtaac gatatcggtt tcatcggtt ccaccagttc 1200
aacaatatcg ctaaaactggt tgcttccaaac tggtacaatc gtcagatcga acgttcctct 1260
cgcaactctgg gttgctcttg ggagttcatc ccgggttgatg acggttgggg tgaacgtccg 1320
ctgtaaatgc tc 1332

<210> 2
<211> 437
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

<400> 2
Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
1 5 10 15
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
20 25 30
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
35 40 45
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
50 55 60
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
65 70 75 80
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
85 90 95
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
100 105 110
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
115 120 125
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
130 135 140
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
145 150 155 160
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
165 170 175
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn

180	185	190
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile		
195	200	205
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu		
210	215	220
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp		
225	230	235
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn		
245	250	255
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg		
260	265	270
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn		
275	280	285
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys		
290	295	300
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg		
305	310	315
Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr		
325	330	335
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile		
340	345	350
Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn		
355	360	365
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn		
370	375	380
Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala		
385	390	395
Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser		
405	410	415
Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp		
420	425	430
Gly Glu Arg Pro Leu		
435		

<210> 3
 <211> 1323
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<400> 3
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 aacatcggtt ctaaaagttaa cttcgatccg atcgacaaga atcagatcca gctgttcaat 180
 ctggaatctt ccaaaatcga agttatcctg aagaatgcta tcgtatacaa ctctatgtac 240
 gaaaacttct ccacccctt ctggatccgt atccccaaat acttcaactc catctctctg 300
 aacaatgaat acaccatcat caactgcatt gaaaacaatt ctgggttggaa agtatctctg 360
 aactacggtg aaatcatctg gactctgcag gacactcagg aaatcaaaca gcgtgttgta 420
 ttcaaatact ctcagatgtat caacatctt gactacatca atcgctggat cttcgttacc 480
 atcaccaaca atcgctgaa taactccaaa atctacatca acggccgtct gatcgaccag 540
 aaaccgatct ccaatctggg taacatccac gcttctaata acatcatgtt caaactggac 600
 ggttgcgtg acactcaccg ctacatctgg atcaaatact tcaatctgtt cgacaaaagaa 660
 ctgaacgaaa aagaaatcaa agacctgtac gacaaccagt ccaattctgg tattctgaaa 720
 gacttctggg gtgactacatc gcagtgacaa aaaccgtact acatgctgaa tctgtacatc 780

ccgaacaaat acgttacgt caacaatgt a ggtatccgc gttacatgt a cctgaaagg 840
ccgcgtggtt ctgttatgac taccaacatc tacctgaact cttccctgt a ccgtggta 900
aaattcatca tcaagaaata cgcgtctgg aacaaggaca atatcggtc aacaatgt 960
cgtgtataca tcaatgttgt agttaagaac aaagaatacc gtctggctac caatgcttct 1020
caggctggtg tagaaaagat cttgtctgct ctggaaatcc cggacgttgg taatctgtct 1080
caggtatgg taatgaaaatc caagaacgac cagggatca ctaacaaatg caaaatgaat 1140
ctgcaggaca acaatggtaa cgatatcggt ttcatcggt tccaccaggta caacaatatc 1200
gctaaactgg ttgcttccaa ctggtacaat cgtcagatcg aacgttcctc tcgcactctg 1260
ggtgcttctt gggagttcat cccgggttcat gacgggttggg gtgaacgtcc gctgtaaagaa 1320
ttc 1323

<210> 4
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

<400> 4
Met Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile
1 5 10 15
Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr
20 25 30
Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp
35 40 45
Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val
50 55 60
Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser
65 70 75 80
Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu
85 90 95
Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp
100 105 110
Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr
115 120 125
Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn
130 135 140
Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn
145 150 155 160
Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
165 170 175
Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met
180 185 190
Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys
195 200 205
Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp
210 215 220
Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly
225 230 235 240
Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp
245 250 255
Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met
260 265 270
Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu
275 280 285

Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala
290 295 300
Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile
305 310 315 320
Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser
325 330 335
Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val
340 345 350
Gly Asn Leu Ser Gln Val Val Met Lys Ser Lys Asn Asp Gln Gly
355 360 365
Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp
370 375 380
Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val
385 390 395 400
Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
405 410 415
Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg
420 425 430
Pro Leu

<210> 5
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<400> 5
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atccctgaacc tgcgctacga atccaaatcac ctgatcgacc tgcgtcgcta cgcttccaaa 120
atcaacatcg gttctaaagt taacttcgat ccgatcgaca agaattcagat ccagctgttc 180
aatctggaaat cttccaaaat cgaagttatc ctgaagaatg ctatcgata caactctatg 240
tagaaaaact tctccacccctc cttctggatc cgtatcccga aataacttcaa ctccatctct 300
ctgaacaatg aatacaccat catcaactgc atggaaaaca attctggttt gaaagtatct 360
ctgaactacg gtgaaatcat ctggactctg caggacactc aggaatcaa acagcgtgtt 420
gtattcaaat actctcagat gatcaacatc tctgactaca tcaatcgctg gatcttcgtt 480
accatcacca acaatcgctt gaataactcc aaaatctaca tcaacggccg tctgatcgac 540
cagaaaccga tctccaatct ggtaacatc cacgcttcta ataacatcat gttcaaactg 600
gacgggttgcgtc gtgacactca ccgctacatc tggatcaaacttcaatct gttcgacaaa 660
gaactgaacg aaaaagaaat caaagacctg tacgacaacc agtccaaattc tggatcctg 720
aaagacttct ggggtgacta cctgcgtac gacaaaccgt actacatgtt gatctgtac 780
gatccgaaca aatacgttga cgtcaacaat gtaggtatcc gcggttatcat gtacctgaaa 840
ggtccgcgtg gttctgttat gactaccaac atctacctga actctccct gtaccgtgtt 900
accaaattca tcatacaagaa atacgcgtct ggtaacaagg acaatatcgt tcgcaacaat 960
gatcgtgtat acatcaatgt tggatctaag aacaaagaat accgtctggc taccaatgtt 1020
tctcaggctg gtgtaaaaa gatcttgcgtc gctctggaaa tcccggtacgt tggtaatctg 1080
tctcaggtag ttgtatgaa atccaaagaac gaccaggta tcaactaacaa atgcaaaatg 1140
aatctgcagg acaacaatgg taacgatatc ggtttcatcg gttccacca gttcaacaat 1200
atcgctaaac tggttgcgttc caactggatc aatcgctaga tcgaacgttc ctctcgact 1260
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gaattc 1326

<210> 6
<211> 435

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

<400> 6

Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser
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Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg
20 25 30
Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile
35 40 45
Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu
50 55 60
Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe
65 70 75 80
Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser
85 90 95
Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly
100 105 110
Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp
115 120 125
Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile
130 135 140
Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn
145 150 155 160
Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp
165 170 175
Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile
180 185 190
Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile
195 200 205
Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys
210 215 220
Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp
225 230 235 240
Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr
245 250 255
Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr
260 265 270
Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr
275 280 285
Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr
290 295 300
Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr
305 310 315 320
Ile Asn Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala
325 330 335
Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp
340 345 350
Val Gly Asn Leu Ser Gln Val Val Met Lys Ser Lys Asn Asp Gln
355 360 365
Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn
370 375 380
Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu

385 390 395 400
Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr
405 410 415
Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
420 425 430
Arg Pro Leu
435

<210> 7
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTB Hc

<400> 7
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gacgggtttg aactgaatga caagaaccag ttcaaactga cctctccgc taactctaag 180
atccgtgtta ctcagaatca gaacatcatc ttcaactccg tattccttggc cttctctgtt 240
tccttcttggc ttcgtatccc gaaatacaag aacgacggta tccagaatata catccacaat 300
gaatacacca tcatacaactg catgaagaat aactctggtt ggaagatctc catccgggt 360
aaccgtatca tctggactct gatcgatatac aacggtaaga ccaaactctgtt attcttcgaa 420
tacaacatcc gtgaagacat ctctgaatac atcaatcgct gttcttcgtt taccatcacc 480
aataacctga acaatgctaa aatctacatc aacggtaaac tggaaatctaa taccgacatc 540
aaagacatcc gtgaaggatcatc cgctaaacgggt gaaatcatct tcaaacttggc cggtgacatc 600
gatcgtagcc agttcatctg gatgaaatac ttctccatct tcaacaccgg actgtctcag 660
tccaaatatcg aagaacggta caagatcccg tcttactccg aataaccttggc agacttctgg 720
ggtaatccgc tggatgtacaa caaagaatac tataatgttca atgctggtaa caagaactct 780
tacatcaaac tgaagaaaaga ctctccgggtt ggtgaaatcc tgactcggtt caaatacaac 840
cagaactcta aatacatcaa ctaccggcgcac ctgtacatcg gtgaaaaggcatcatccgt 900
cgcaaatcta actctcagtc catcaatgtt gacatcgatc gtaaaagaaga ctacatctac 960
ctggacttct tcaacctgaa tcaggaatgg cgtgtataca cctacaaggtt cttcaagaaa 1020
gaagaagaaa agctttccct ggctccggatc tctgattccg acgaaactcttca caacaccatc 1080
cagatcaaag aatacgacga acagccgacc tacttttgc agctgctgtt caagaaagat 1140
gaagaatcta ctgacgaaat cggtctgttccg ggtatccacc gtttcttacga atctggatc 1200
gtattcgaag aatacaaaaga ctacttctgc atctccaaat ggtaccttggaa ggaagttaaa 1260
cgcaaaccgtt acaacctgaa actgggttgc aattggcagt tcataccggaa agacgaaggt 1320
tggaccgaat agtaagaatt c 1341

<210> 8
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTB Hc

<400> 8
Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn
1 5 10 15
Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala
20 25 30
Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe

35	40	45														
Lys	Leu	Thr	Ser	Ser	Ala	Asn	Ser	Lys	Ile	Arg	Val	Thr	Gln	Asn	Gln	
50					55					60						
Asn	Ile	Ile	Phe	Asn	Ser	Val	Phe	Leu	Asp	Phe	Ser	Val	Ser	Phe	Trp	
65					70					75					80	
Ile	Arg	Ile	Pro	Lys	Tyr	Lys	Asn	Asp	Gly	Ile	Gln	Asn	Tyr	Ile	His	
					85					90					95	
Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Lys	Asn	Asn	Ser	Gly	Trp	Lys	
					100				105					110		
Ile	Ser	Ile	Arg	Gly	Asn	Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Ile	Asn	
					115				120					125		
Gly	Lys	Thr	Lys	Ser	Val	Phe	Phe	Glu	Tyr	Asn	Ile	Arg	Glu	Asp	Ile	
					130				135					140		
Ser	Glu	Tyr	Ile	Asn	Arg	Trp	Phe	Phe	Val	Thr	Ile	Thr	Asn	Asn	Leu	
145					150					155					160	
Asn	Asn	Ala	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	Leu	Glu	Ser	Asn	Thr	Asp	
					165				170					175		
Ile	Lys	Asp	Ile	Arg	Glu	Val	Ile	Ala	Asn	Gly	Glu	Ile	Phe	Lys		
					180				185					190		
Leu	Asp	Gly	Asp	Ile	Asp	Arg	Thr	Gln	Phe	Ile	Trp	Met	Lys	Tyr	Phe	
					195				200					205		
Ser	Ile	Phe	Asn	Thr	Glu	Leu	Ser	Gln	Ser	Asn	Ile	Glu	Glu	Arg	Tyr	
					210				215					220		
Lys	Ile	Gln	Ser	Tyr	Ser	Glu	Tyr	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Pro	
					225				230					240		
Leu	Met	Tyr	Asn	Lys	Glu	Tyr	Tyr	Met	Phe	Asn	Ala	Gly	Asn	Lys	Asn	
					245				250					255		
Ser	Tyr	Ile	Lys	Leu	Lys	Asp	Ser	Pro	Val	Gly	Glu	Ile	Leu	Thr		
					260				265					270		
Arg	Ser	Lys	Tyr	Asn	Gln	Asn	Ser	Lys	Tyr	Ile	Asn	Tyr	Arg	Asp	Leu	
					275				280					285		
Tyr	Ile	Gly	Glu	Lys	Phe	Ile	Ile	Arg	Arg	Lys	Ser	Asn	Ser	Gln	Ser	
					290				295					300		
Ile	Asn	Asp	Asp	Ile	Val	Arg	Lys	Glu	Asp	Tyr	Ile	Tyr	Leu	Asp	Phe	
					305				310					320		
Phe	Asn	Leu	Asn	Gln	Glu	Trp	Arg	Val	Tyr	Thr	Tyr	Lys	Tyr	Phe	Lys	
					325				330					335		
Lys	Glu	Glu	Glu	Lys	Leu	Phe	Leu	Ala	Pro	Ile	Ser	Asp	Ser	Asp	Glu	
					340				345					350		
Leu	Tyr	Asn	Thr	Ile	Gln	Ile	Lys	Glu	Tyr	Asp	Glu	Gln	Pro	Thr	Tyr	
					355				360					365		
Ser	Cys	Gln	Leu	Leu	Phe	Lys	Lys	Asp	Glu	Glu	Ser	Thr	Asp	Glu	Ile	
					370				375					380		
Gly	Leu	Ile	Gly	Ile	His	Arg	Phe	Tyr	Glu	Ser	Gly	Ile	Val	Phe	Glu	
					385				390					395		
Glu	Tyr	Lys	Asp	Tyr	Phe	Cys	Ile	Ser	Lys	Trp	Tyr	Leu	Lys	Glu	Val	
					405				410					415		
Lys	Arg	Lys	Pro	Tyr	Asn	Leu	Lys	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile	
					420				425					430		
Pro	Lys	Asp	Glu	Gly	Trp	Thr	Glu									
					435				440							

<210> 9
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTC1 Hc

<400> 9

gaattcacga tgaccatccc attcaacatc ttctcctaca ccaacaactc cctgttgaag 60
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cgtaagaaca ccttggtcga cacctccgg tacaacgccc aggtctccga ggagggtgac 180
gtccagctga acccaatctt cccattcgac ttcaagctgg gttctccgg tgaggacaga 240
ggttaaggta tcgtcaccca gaacgagaac atcgcttaca actccatgtt cgagtccttc 300
tccatctcct tctggatcag aatcaacaag tgggtctcca acttgccagg ttacaccatc 360
atcgactccg tcaagaacaa ctccgggttgg tccatcggtt tcatctccaa cttcctggtc 420
ttcacccctga agcagaacga ggactccgag cagtcatca acttctccta cgacatctcc 480
aacaacgctc ctggttacaa caagtggttc ttctgttaccg tcaccaacaa catgatgggt 540
aacatgaaga tctacatcaa cgtaagctg atcgacacca tcaaggtcaa ggagttgacc 600
ggtatcaact tctccaagac catcacccctc gagatcaaca agatcccaga caccggcttg 660
atcacctccg actccgacaa catcaacatcg tggatccgtg acttcttacat cttcgccaag 720
gagttggacg gtaaggacat caacatccct ttcaactctc tgcagtacac caacgtcgtc 780
aaggactact gggtaacga cctgagatac aacaaggagt actacatgtt caacatcgac 840
tacattgaaca gatacatgtt cgccaaactcc agacagatcg tcttcaacac cagacgtaac 900
aacaacgact tcaacgaggg ttacaagatc atcatcaagc gtatcagagg taacaccaac 960
gacaccagag tcagagggtgg tgacatccctg tacttcgaca tgactatcaa caacaaggcc 1020
tacaacccctgt tcatgaagaa cgagaccatcg tacgcccaca accactccac cgaggacatc 1080
tacgcccattcg gtctgcgtga gcagaccaag gacatcaacg acaacatcat cttccagatc 1140
cagccaatgaa acaacactta ctactacgct tcccagatct tcaagtccaa cttcaacgggt 1200
gagaacatct ccggtatctg ttccatcggtt acctacagat tccgtctggg tggtgactgg 1260
tacagacaca actacttggt tccaactgtc aagcagggtt actacgcctc cttgctggag 1320
tccacttcca cccactgggg attcgccccca gtctccgagt aataggaatt c 1371

<210> 10

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTC1 Hc

<400> 10

Met	Thr	Ile	Pro	Phe	Asn	Ile	Phe	Ser	Tyr	Thr	Asn	Asn	Ser	Leu	Leu
1				5				10					15		
Lys	Asp	Ile	Ile	Asn	Glu	Tyr	Phe	Asn	Asn	Ile	Asn	Asp	Ser	Lys	Ile
					20				25				30		
Leu	Ser	Leu	Gln	Asn	Arg	Lys	Asn	Thr	Leu	Val	Asp	Thr	Ser	Gly	Tyr
					35				40			45			
Asn	Ala	Glu	Val	Ser	Glu	Glu	Gly	Asp	Val	Gln	Leu	Asn	Pro	Ile	Phe
					50			55			60				
Pro	Phe	Asp	Phe	Lys	Leu	Gly	Ser	Ser	Gly	Glu	Asp	Arg	Gly	Lys	Val
					65			70			75		80		
Ile	Val	Thr	Gln	Asn	Glu	Asn	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Ser
					85			90				95			
Phe	Ser	Ile	Ser	Phe	Trp	Ile	Arg	Ile	Asn	Lys	Trp	Val	Ser	Asn	Leu
					100			105			110				
Pro	Gly	Tyr	Thr	Ile	Ile	Asp	Ser	Val	Lys	Asn	Asn	Ser	Gly	Trp	Ser
					115			120			125				
Ile	Gly	Ile	Ile	Ser	Asn	Phe	Leu	Val	Phe	Thr	Leu	Lys	Gln	Asn	Glu
					130			135			140				

Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn Asn Ala
 145 150 155 160
 Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn Met Met
 165 170 175
 Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys
 180 185 190
 Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu
 195 200 205
 Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn
 210 215 220
 Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp
 225 230 235 240
 Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val
 245 250 255
 Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr
 260 265 270
 Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser Arg
 275 280 285
 Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn Glu Gly
 290 295 300
 Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp Thr Arg
 305 310 315 320
 Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn Asn Lys
 325 330 335
 Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp Asn His
 340 345 350
 Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr Lys Asp
 355 360 365
 Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn Thr Tyr
 370 375 380
 Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu Asn Ile
 385 390 395 400
 Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp
 405 410 415
 Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr
 420 425 430
 Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val
 435 440 445
 Ser Glu
 450

<210> 11
 <211> 1374
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTD Hc

<400> 11
 gaattcacga tgcgttgaa ggctaaggtc aacgagtcct tcgagaacac catgccattc 60
 aacatcttct cctacaccaa caactccttg ttgaaggaca tcatcaacga gtacttcaac 120
 tccatcaacg actccaagat cttgtccttg cagaacaaga agaacgcctt ggtcgacacc 180
 tccggttaca acggcgaggt cagagtcggc gacaacgtcc agttgaacac catctacacc 240
 aacgacttca agttgtcctc ttccggtgac aagatcatcg tcaacttcaa caacaacatc 300
 ttgtactccg ccatctacga gaactcctct gtctccttct ggatcaagat ctccaaaggac 360

ttgaccaact cccacaacga gtacaccatc atcaactcca tcgagcagaa ctccgggtgg 420
aagggtgtta cccgtaacgg taacatcgag tggatcttgc aggacgtcaa ccgtaaatgtac 480
aagtccctga ttttcgacta ctccgagtcc ttgtcccaca ccggttacac caacaagtgg 540
ttttcgatca ccatcaccaa caacatcatg gtttacatga agttgtacat caacggtgag 600
ttgaaggagt cccagaagat cgaggacctg gacgaggtca agctggacaa gaccatcgtc 660
ttcggtatcg acgagaacat cgacgagaac cagatgtgt gatccgtga cttcaacatc 720
tttccaagg agctgtccaa cgaggacatc aacatcgatc acgagggtca gatctgagg 780
aacgtcatca aggactactg ggttaaccca ctgaagttcg acaccgagta ctacatcatc 840
aacgacaact acatcgaccg ttacatcgcc ccagagtcca acgtcctgt cctggtccag 900
taccctgacc gttccaagct gtacaccgg aaccctatca ccatcaagtc cgttccgac 960
aagaaccctt actcccgat cctgaacggt gacaacatca tcctgcacat gctgtacaac 1020
tcccgtaagt acatgatcat ccgtgacacc gacaccatct acgcccacca gggtggtgac 1080
tgttcccaga actgtgtcta cggccctgaa ctgcagtcca acctgggtaa ctacgggtatc 1140
ggtatcttct ccatcaagaa catcgatctcc aagaacaagt actgttccca gatcttctcc 1200
tccttccgtg agaacaccat gctgctggcc gacatctaca agccttggcg tttcttcttc 1260
aagaacgcct acactcctgt cggcgtcacc aactacgaga ccaagctgt gtccacctcc 1320
tccttctgga agttcatctc ccgtgaccca ggttgggtcg agtaatagga attc 1374

<210> 12
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTD Hc

<400> 12
Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro
1 5 10 15
Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile
20 25 30
Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln
35 40 45
Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val
50 55 60
Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe
65 70 75 80
Lys Leu Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn
85 90 95
Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile
100 105 110
Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile
115 120 125
Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly
130 135 140
Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu
145 150 155 160
Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys
165 170 175
Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu
180 185 190
Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp
195 200 205
Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile
210 215 220
Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys

225	230	235	240												
Glu	Leu	Ser	Asn	Glu	Asp	Ile	Asn	Ile	Val	Tyr	Glu	Gly	Gln	Ile	Leu
245				250										255	
Arg	Asn	Val	Ile	Lys	Asp	Tyr	Trp	Gly	Asn	Pro	Leu	Lys	Phe	Asp	Thr
260				265									270		
Glu	Tyr	Tyr	Ile	Ile	Asn	Asp	Asn	Tyr	Ile	Asp	Arg	Tyr	Ile	Ala	Pro
275				280								285			
Glu	Ser	Asn	Val	Leu	Val	Leu	Val	Gln	Tyr	Pro	Asp	Arg	Ser	Lys	Leu
290				295							300				
Tyr	Thr	Gly	Asn	Pro	Ile	Thr	Ile	Lys	Ser	Val	Ser	Asp	Lys	Asn	Pro
305				310						315			320		
Tyr	Ser	Arg	Ile	Leu	Asn	Gly	Asp	Asn	Ile	Ile	Leu	His	Met	Leu	Tyr
325				330								335			
Asn	Ser	Arg	Lys	Tyr	Met	Ile	Ile	Arg	Asp	Thr	Asp	Thr	Ile	Tyr	Ala
340				345								350			
Thr	Gln	Gly	Gly	Asp	Cys	Ser	Gln	Asn	Cys	Val	Tyr	Ala	Leu	Lys	Leu
355				360							365				
Gln	Ser	Asn	Leu	Gly	Asn	Tyr	Gly	Ile	Gly	Ile	Phe	Ser	Ile	Lys	Asn
370				375							380				
Ile	Val	Ser	Lys	Asn	Lys	Tyr	Cys	Ser	Gln	Ile	Phe	Ser	Ser	Phe	Arg
385				390						395			400		
Glu	Asn	Thr	Met	Leu	Leu	Ala	Asp	Ile	Tyr	Lys	Pro	Trp	Arg	Phe	Ser
405				410									415		
Phe	Lys	Asn	Ala	Tyr	Thr	Pro	Val	Ala	Val	Thr	Asn	Tyr	Glu	Thr	Lys
420				425								430			
Leu	Leu	Ser	Thr	Ser	Ser	Phe	Trp	Lys	Phe	Ile	Ser	Arg	Asp	Pro	Gly
435				440							445				
Trp	Val	Glu													
450															

<210> 13
<211> 1400
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTe Hc

<400> 13
gaattcacca tgggagagag tcagcaagaa ctaaattcta tggtaactga taccctaaat 60
aatagtattc ctttaagct ttcttcttat acagatgata aaattttaat ttccctacttc 120
aacaagttct tcaagagaat taagtcttct tccgtttaa acatgagata caagaatgat 180
aaatacgtcg acacttccgg ttacgactcc aatatcaaca ttaacggtga cgtgtacaag 240
tacccaacta acaaaaacca attcggtatac tacaacgaca agcttactga gctgaacatc 300
tctaaaacg actacattat ctacgacaac aagtacaaga acttctctat ttcttctgg 360
gtcaggattc ctaactacga caacaagatc gtcaacgtta acaacgagta cactatcatc 420
aactgtatga gagacaacaa ctccgggtgg aaggtctctc ttaaccaccaa cgagatcatt 480
tggaccttgc aagacaacgc aggtattaaac caaaaagttag cattcaacta cggttaacgca 540
aacggtattt ctgactacat caacaagtgg atttcgtca ctatcaacta cgacagattta 600
ggtgactcta agctttacat taacggtaac ttaatcgacc aaaagtccat tttaaactta 660
ggtaacattc acgtttctga caacatctta ttcaagatcg ttaactgcag ttacaccaga 720
tacattggca ttagataactt caacattttc gacaaggagt tagacgagac cgagattcaa 780
actttataca gcaacgaacc taacaccaat atttgaagg acttctgggg taactacttg 840
cttacgaca aggaatacta ctatcaaac gtgttaaagc caaaacaactt cattgatagg 900
agaaaggatt ctacttaag cattaacaac atcagaagca ctattcttt agctaacaga 960
ttatactctg gtatcaaggt taagatccaa agagttaaaca acttctctac taacgataac 1020

cttggtagaa agaacgatca ggtctatatt aacttcgtcg ctagcaagac tcacttattc 1080
ccattatatg ctgataccgc taccaccaac aaggagaaga ccatcaagat ctcctcctct 1140
ggcaacagat ttaaccaagt cgtcggtatg aactccgtcg gtaacaactg taccatgaac 1200
ttaaaaata ataatggaaa taatattggg ttgttaggtt tcaaggcaga tactgttagtt 1260
gctagtactt ggtattatac ccacatgaga gatcacacca acagcaatgg atgttttgg 1320
aactttatcc ctgaagaaca tggatggcaa gaaaaataat agggatccgc ggccgcacgc 1380
gtcccgac tagtgaattc 1400

<210> 14
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTe Hc

<400> 14
Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp Thr Leu
1 5 10 15
Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp Lys Ile
20 25 30
Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser Ser Ser
35 40 45
Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr Ser Gly
50 55 60
Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr Pro Thr
65 70 75 80
Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu Leu Asn
85 90 95
Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys Asn Phe
100 105 110
Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys Ile Val
115 120 125
Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp Asn Asn
130 135 140
Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu
145 150 155 160
Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn
165 170 175
Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile
180 185 190
Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu
195 200 205
Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp
210 215 220
Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly
225 230 235 240
Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile
245 250 255
Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys Asp Phe
260 265 270
Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val
275 280 285
Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser
290 295 300
Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser

305	310	315	320
Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp			
325	330	335	
Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser			
340	345	350	
Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys			
355	360	365	
Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn Gln Val			
370	375	380	
Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe Lys Asn			
385	390	395	400
Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr Val			
405	410	415	
Val Ala Ser Thr Trp Tyr Tyr His Met Arg Asp His Thr Asn Ser			
420	425	430	
Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln Glu			
435	440	445	
Lys			

<210> 15
 <211> 1317
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTF Hc

<400> 15
 gaattcacga tggcctacac caacgacaag atcctgatct tgtacttcaa caagctgtac 60
 aagaagatca aggacaactc catcttggac atgagatacg aaaacaataa gttcatcgac 120
 atctccggtt acggttccaa catctccatc aacggtgacg tctacatcta ctccaccaat 180
 agaaaaccagt tcggaatcta ctccctccaag ccttccgagg tcaacatcgc tcagaacaac 240
 gacatcatct acaacgaaag ataccagaac ttctccatct cttctgggt ccgtatccca 300
 aagtacttca acaaggtaaa cctgaataac gagtacacca tcatcgactg catccgtAAC 360
 aataactccg gatggaaagat ctcccctgaac tacaacaaga tcatctggac cctgcaggac 420
 accgcggta acaatcagaa gttggtcttc aactacaccc agatgatctc catctccgac 480
 tacatcaaca agtggatctt cgtcaccatc accaataacc gtttgggaaa ctccagaatc 540
 tacatcaacg gtaacttgat cgacgagaag tccatctcca acttgggtga catccacgac 600
 tccgacaaca ttttgttcaa gatcgctgggt tgtaacgaca cccgttacgt cgggatccgt 660
 tacttcaaag tcttcgacac tgagttgggt aagaccgaga tcgagacctt gtactccgac 720
 gagcctgacc catccatcct gaaggacttc tgggtaact acctgctgtca caacaaacgt 780
 tactacttgc tgaacttgat ggttccatca cccagaactc caacttcttg 840
 aacatcaacc agcagagagg tgtctaccag aagccaaaca tcttctccaa caccagattg 900
 tacaccggag tcgaggtcat tatcagaaag aacggatcta ctgatatttc caacaccgat 960
 aacttcgtca gaaagaacga tctggcttac atcaacgttg tcgacagaga tgtcgaatac 1020
 cgtctgtacg ccgatatactc tattcgccaaa cctgaaaaga tcattcaaggt gatccgtacc 1080
 tcttaactcta acaactctct ggacaaatc atcgcatgg actccatcg taataactgt 1140
 accatgaact tccagaaacaa caacggtgaa aacatcggtt tggtgggtt ccactccaa 1200
 aacttggtgc cttcctcctg gtactacaac aacatccgtaa agaacaccc tcccaacgg 1260
 tgcttctgggt ctttcatctc caaggagcac ggttggcagg agaactaata ggaattc 1317

<210> 16
 <211> 432
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTF Hc

<400> 16

Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
1 5 10 15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
20 25 30
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
35 40 45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
50 55 60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
65 70 75 80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
85 90 95
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
100 105 110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
115 120 125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
130 135 140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
145 150 155 160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
165 170 175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
180 185 190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
195 200 205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
210 215 220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
225 230 235 240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
245 250 255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
260 265 270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
275 280 285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
290 295 300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
305 310 315 320
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
325 330 335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
340 345 350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
355 360 365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
370 375 380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
385 390 395 400
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn

405 410 415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
420 425 430

<210> 17
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTG Hc

<400> 17
gaattcacga tgaaggacac catcctgatc caggtcttca acaactacat ctccaacatc 60
tcctccaaacg ccatcctgtc cctgtcctac cgtgggtgtc gtctgatcga ctccctccgt 120
tacggagcca ccatgaacgt cggttccgac gtcatcttca acgacatcgg taacgggtcag 180
ttcaagctga acaactccga gaactccaac atcaccgccc accagtccaa gttcgctgtc 240
tacgactcca tggcgacaa cttctccatc aacttctggg tccgtacccc aaagtacaac 300
aacaacgaca tccagaccta cctgcagaac gagtacacca tcatctcctg tatcaagaac 360
gactccgggtt ggaagggtctc catcaaggga aaccgttatca tctggaccct gatgacgtc 420
aacgccaagt ccaagttccat ctcttcgag tactccatca aggacaacat ctccgactac 480
atcaacaagt ggttctccat caccatcacc aacgaccgtc tggtaacgc caacatctac 540
atcaacgggtt ccctgaagaa gtccgagaag atcctgaacc tggaccgtat caactcctcc 600
aacgacatcg acttcaagct gatcaactgt accgacacca ccaagttcgt ctggatcaag 660
gacttcaaca tcttcggtcg tgagctgaac gccaccgagg tctcctccct gtactggatc 720
cagtcctcca ccaacaccct gaaggacttc tggggaaacc cactgcgtt cggacacccag 780
tactacctgt tcaaccaggg tatgcagaac atctacatca agtacttctc caaggcctcc 840
atgggtgaga cccgccttcg taccaacttc aacaacgccc ccatcaacta ccagaacctg 900
tacctgggtc tgcgttcat catcaagaag gcctccaact cccgttaacat caacaacgac 960
aacatcgtcc gtgaggggtga ctacatctac ctgaacatcg acaacatctc cggcggatcc 1020
taccgtgtct acgtcctggt caactccaag gagatccaga cccagctgtt cctggcccca 1080
atcaacgacg accctacctt ctacgacgtc ctgcagatca agaagtacta cggaaagacc 1140
acctacaact gtcagatcct gtgcgagaag gacaccaaga cttcggact gttcggtatc 1200
ggtaagttcg tcaaggacta cggttacgtc tgggacacct acgacaacta cttctgtatc 1260
tcccaagtggt acctgcgtcg tatctccgag aacatcaaca agctgcgtct gggatgtaac 1320
tggcagttca tcccagtcga cgagggttgg accgagtaat aggaattc 1368

<210> 18
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTG Hc

<400> 18
Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn
1 5 10 15
Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu
20 25 30
Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val
35 40 45
Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu
50 55 60
Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser

65	70	75	80
Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr			
85	90	95	
Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr Ile Ile			
100	105	110	
Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys Gly Asn			
115	120	125	
Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys Ser Ile			
130	135	140	
Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile Asn Lys			
145	150	155	160
Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala Asn Ile			
165	170	175	
Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn Leu Asp			
180	185	190	
Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn Cys Thr			
195	200	205	
Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe Gly Arg			
210	215	220	
Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser			
225	230	235	240
Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr			
245	250	255	
Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr			
260	265	270	
Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn			
275	280	285	
Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile			
290	295	300	
Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val			
305	310	315	320
Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu			
325	330	335	
Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln			
340	345	350	
Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu			
355	360	365	
Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu			
370	375	380	
Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly Lys Phe			
385	390	395	400
Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr Phe Cys			
405	410	415	
Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn Lys Leu			
420	425	430	
Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly Trp Thr			
435	440	445	
Glu			

<210> 19
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hn

<400> 19

atggctctga acgacacctgtg catcaaagtt aacaactggg acctgttctt ctccccgtct 60
gaagacaact tcactaacga cctgaacaaa ggcgaagaaa tcaccccgaa cactaacatc 120
gaagctgctg aagaaaaacat ctctctggac ctgatccagc agtactacct gacttcaac 180
ttcgacaaacg aaccggaaaa catctccatc gaaaacctgt cttccgacat catcggtcag 240
ctgaaactga tgccgaacat cgaacgcttc ccgaacggca agaaatacga actggacaaa 300
tacaccatgt tccactacct gcgtgctca gattcgaac acggtaaatac tcgtatcgct 360
ctgactaact ccgttaacga agctctgctg aaccctgtc gcgttacac cttcttctct 420
tccgactacg ttaagaaagt taacaaagct actgaagctg ctatgttctt gggttgggtt 480
gaacagctgg ttacgactt caccgacgaa acttctgaag ttccaccac tgacaaaatc 540
gctgacatca ctatcatcat cccgtacatc ggccggctc tgaacatcgtaa catgctg 600
tacaaagacg acttcgttgg tgctctgatc ttctctggcg ctgttatcct gctgaaattc 660
atcccgaaaa tcgctatccc gttctgggt accttcgtc tggttcccta catcgctaac 720
aaagttctga ctgttacagac catcgacaaac gctctgtcta aacgtaaacgaaaatggac 780
gaagtttaca aatacatcgt tactaactgg ctggctaaag ttaacactca gatgacactg 840
atccgtaaga agatgaaaga agctctggaa aaccaggctg aagctactaa agctatcatc 900
aactaccagt acaaccagta caccgaagaa gaaaagaaca acatcaactt caacatcgat 960
gacctgtcct ctaaaactgaa cgaatccatc aacaagcta tgatcaacat caacaaattc 1020
ctgaaccagt gctcttttc ctacctgatc aactctatga tcccgatcgg cgtaaacgc 1080
ctgaaagact tcgacgttc cctgaaagac gctctgtca aatacatccg tgacaactac 1140
ggtaactctga tcggccaggt tgaccgtctg aaagacaagg ttaacaacac cctgtctact 1200
gacatcccgt tccagctgtc caaatacgtt gacaaccagt aa 1242

<210> 20

<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hn

<400> 20

Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
1 5 10 15
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
20 25 30
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
35 40 45
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
50 55 60
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
65 70 75 80
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr
85 90 95
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
100 105 110
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
115 120 125
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
130 135 140
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
145 150 155 160
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
165 170 175

Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Pro Tyr Ile Gly Pro
 180 185 190
 Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala
 195 200 205
 Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile
 210 215 220
 Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn
 225 230 235 240
 Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn
 245 250 255
 Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala
 260 265 270
 Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala
 275 280 285
 Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr
 290 295 300
 Asn Gln Tyr Thr Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp
 305 310 315 320
 Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn
 325 330 335
 Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser
 340 345 350
 Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu
 355 360 365
 Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile
 370 375 380
 Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr
 385 390 395 400
 Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
 405 410

<210> 21
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTB Hn

<400> 21
 atggctccag gaatctgtat cgacgtcgac aacgaggact ttttcttcat cgctgacaag 60
 aactccttct ccgacgactt gtccaaagaac gagagaatcg agtacaacac ccagtcac 120
 tacatcgaga acgacttccc aatcaacgag ttgatcttgg acaccgactt gatctccaag 180
 atcgagttgc catccgagaa caccgagtc ttgactgact tcaacgtcga cgtcccagtc 240
 tacgagaagc aaccagctat caagaagatt ttcaccgacg agaacaccat cttccaatac 300
 ctgtactctc agaccttccc tttggacatc agagacatct ctttgacctc ttccttcgac 360
 gacgcctgc ttttctccaa caaggtctac tccttcttcc ccatggacta catcaagact 420
 gctaaacaagg tcgtcgaggc cggttttttc gctgggtggg tcaaggcagat cgtcaacgat 480
 ttctgtatcg aggctaaaca gttccaaacacc atggacaaga ttgcccacat ctccttgatt 540
 gtcccataca tcggtttggc cttgaacgtc ggtaacgaga cccccaagggg taacttcgag 600
 aacgctttcg agatcgctgg tgcctccatc ttgtttggagt tcatcccaga gttgttgc 660
 ccagtcgtcg gtgccttctt gttggagtc tacatcgaca acaagaacaa gatcatcaag 720
 accatcgaca acgcttgac caagagaaac gagaagtggt cggacatgtt cggtttgc 780
 gtcgccccat ggttgtccac cgtcaacacc caatttaca ccatcaaggg gggatgtac 840
 aaggcccttga actaccaggc ccaagctttg gaggagatca tcaagtacag atacaacatc 900
 tactccgaga aggagaagtc caacattaaac atcgacttca acgacatcaa ctccaaagctg 960

aacgagggtta ttaaccaggc catcgacaac atcaacaact tcatcaacgg ttgttccgtc 1020
tcctacttga tgaagaagat gattccattt gccgtcgaga agttgttggc cttcgacaac 1080
accctgaaga agaacttggc gaactacatc gacgagaaca agttgtactt gatcggttcc 1140
gctgagtacg agaagtccaa ggtcaacaag tacttgaaga ccatcatgcc attcgacttg 1200
tccatctaca ccaacgacac catcttgatc gagatgttct aa 1242

<210> 22
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTB Hn

<400> 22
Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe
1 5 10 15
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg
20 25 30
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile
35 40 45
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro
50 55 60
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val
65 70 75 80
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr
85 90 95
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp
100 105 110
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys
115 120 125
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val
130 135 140
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp
145 150 155 160
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp
165 170 175
Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn
180 185 190
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala
195 200 205
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly
210 215 220
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys
225 230 235 240
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met
245 250 255
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe
260 265 270
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
275 280 285
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
290 295 300
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
305 310 315 320
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn

325	330	335	
Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val			
340	345	350	
Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn			
355	360	365	
Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu			
370	375	380	
Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu			
385	390	395	400
Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe			
405	410		

```
<210> 23
<211> 1200
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic construct based on BoNTC1 Hn

<400> 23
atgtccctgt aacaacaagac ccttgactgt agagagctgc tggtaagaa cactgacctg 60
ccattcatcg gtgacatcg tgacgtgaag actgacatct tcctgcgtaa ggacatcaac 120
gaggagactg aggtgatcta ctacccagac aacgtgtca tagaccaagt gatcctca 180
aagaacacctt ccgagcatgg acaactagac ctgctctacc ctgttatcga cagtgagagt 240
gagatcctgc caggggagaa tcaagtcttc taacgacaacc gtaccaggaa cgtggactac 300
ctgaactcct actactaccc agagtctcag aagctgagtg acaacgtgga ggacttcact 360
ttcacgcgtt caatcgagga ggctctggac aacagtgcac aggtgtacac ttacttcct 420
accctggcta acaaggtgaa tgccgggttg caaggtggtc tggtccgtat gtggggcaaac 480
gacgtggttt aggacttcac taccacatc ctgcgttaagg acacactgga caagatctca 540
gatgtgtcag ctatcatccc ctacatcgga cccgcactga acatctccaa ctctgtgcgt 600
cgtggaaact tcactgaggc attcgcagtc actgggtgtca ccatctgc ggaggcattc 660
cctgagttca caatccctgc tctgggtgca ttcgtgtatct acagtaaggt ccaggagcga 720
aacgagatca tcaagaccat cgacaactgt ctggagcaga ggtcaagag atggaaggac 780
tcctacgagt ggatgtatggg aacgtggttg tccaggatca tcaccaggat caacaacatc 840
tcctaccaga tgtacgactc cctgaactac caggcagggtg caatcaaggc taagatcgac 900
ctggagttaca agaagtactc cggaaagcgc aaggagaaca tcaagagcca gggttggaaac 960
ctgaagaaca gtctggacgt caagatctcg gaggcaatga acaacatcaa caagttcatc 1020
cgagagtgtct ccgtcaccta cctgttcaag aacatgctgc ctaaggatcat cgacgagctg 1080
aacgagttcg accaaaacac caaggcaaag ctgatcaacc tgatcgactc ccataacatc 1140
atccctggtcg gtgaggtcga caagctgaag gcaaaggtaa acaacagctt ccagaactaa 1200

<210> 24
<211> 399
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTC Hn

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<400> 24
Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
  1           5           10          15
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp

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20	25	30	
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr			
35	40	45	
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser			
50	55	60	
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser			
65	70	75	80
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln			
85	90	95	
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Leu Glu Ser Gln Lys Leu			
100	105	110	
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala			
115	120	125	
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn			
130	135	140	
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn			
145	150	155	160
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu			
165	170	175	
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala			
180	185	190	
Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe			
195	200	205	
Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr			
210	215	220	
Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg			
225	230	235	240
Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys			
245	250	255	
Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg			
260	265	270	
Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu			
275	280	285	
Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys			
290	295	300	
Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn			
305	310	315	320
Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile			
325	330	335	
Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met			
340	345	350	
Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys			
355	360	365	
Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly			
370	375	380	
Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn			
385	390	395	

<210> 25

<211> 1161

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTD Hn

<400> 25

atggccaact cccgtgacga ctccacactgc atcaaggtca agaacaacag actgccatac 60
gttgcgaca aggactccat ctcccaggag atcttcgaga acaagatcat caccgacgag 120
accaacgttc aaaactactc cgacaagttc tctttggacg agtccatcct ggacggtcag 180
gtcccaatca acccagagat cgtcgaccca ctgttgccaa acgtcaacat ggagccattg 240
aacttgcag gtgaggagat cgtcttctac gacgacatca ccaagtagt cgactacttg 300
aactcctact actacttgg a g t c t c a a a a g t t c t a a c a a c g t c g a g a a c a t c a c c t t g 360
accacactccg tcgaggaggc ctgggttac tctaacaaga tctacacctt cctgccatcc 420
ttggctgaga aggttaacaa gggtgttcaa gctgggttgc ttctgaactg ggccaacgag 480
gtcgtcgagg acttcaccac caacatcatg aagaaggaca ccctggacaa gatctccgac 540
gtctccgtca tcatccata catcggtcca gccttgaaca tcggttaactc cgccctgaga 600
ggttaactca accaggcctt cgccaccgc ggtgtcgct tcctgctgga gggttccca 660
gaggtcacca tcccagccct gggtgtcttc accttctact cctccatcca ggagagagag 720
aagatcatca agaccatcga gaactgcttg gaggcagagag tcaagagatg gaaggactcc 780
taccagtgg a t g g t t c c a a c t g c t g t c a g a a t c a c c a c c a a t t c a a c c a c a c 840
taccagatgt acgactccct gtcttaccag gccgacgcca tcaaggccaa gatgacactg 900
gagtaacaaga agtactccgg ttccgacaag gagaacatca agtcccaggt cgagaacctg 960
aagaactcct tggacgtcaa gatctccgag gccatgaaca acatcaacaa gttcatccgt 1020
gagtgttccg tcacctacct gttcaagaac atgctccaa aggtcatcga cgagctgaac 1080
aagttcgacc tgagaaccaa gaccgagctg atcaacctga tcgactccca caacatcatc 1140
ctggttggtg aggttgacta a 1161

<210> 26

<211> 386

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTD Hn

<400> 26

Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
1 5 10 15
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
20 25 30
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
35 40 45
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
50 55 60
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
65 70 75 80
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
85 90 95
Val Asp Tyr Leu Asn Ser Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
100 105 110
Asn Asn Val Glu Asn Ile Thr Leu Thr Ser Val Glu Glu Ala Leu
115 120 125
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
130 135 140
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145 150 155 160
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
165 170 175
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
180 185 190
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala

195	200	205	
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro	Glu Phe Thr Ile		
210	215	220	
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile	Gln Glu Arg Glu		
225	230	235	240
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln	Arg Val Lys Arg		
245	250	255	
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp	Leu Ser Arg Ile		
260	265	270	
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr	Asp Ser Leu Ser		
275	280	285	
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu	Glu Tyr Lys Lys		
290	295	300	
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln	Val Glu Asn Leu		
305	310	315	320
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met	Asn Asn Ile Asn		
325	330	335	
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe	Lys Asn Met Leu		
340	345	350	
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu	Arg Thr Lys Thr		
355	360	365	
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile	Leu Val Gly Glu		
370	375	380	
Val Asp			
385			

<210> 27

<211> 1149

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTE Hn

<400> 27

atgtccatct gcatcgagat caacaacgggt gagctgttct tcgtggcttc cgagaacagt 60
 tacaacgatg acaacatcaa cactcctaag gagattgacg acaccgtcac ttctaaacaac 120
 aactacgaaa acgacctgga ccaggtcatac ctaaacttca actccgagtc cgcccttggt 180
 ctgtccgacg agaagctgaa cctgaccatc cagaacgacg cttacatccc aaagtacgac 240
 tccaaacggta catccgatata cgagcagcat gacgttaacgt agcttaacgt cttttctac 300
 ttagacgctc agaagggtgcc cgagggttag aacaacgtca atctcacctc ttcaattgac 360
 acagccttgt tggagcagcc taagatctac accttcttct cctccgaggt catcaacaac 420
 gtcaacaagc ctgtgcaggc cgattgttc gtaagctgga ttcagcagggt gtttagtagac 480
 ttcaactactg aggctaacca gaagtccact gttgacaaga tcgctgacat ctccatgtc 540
 gtcccatata tcggctctggc tctgaacatc ggcaacgagg cacagaaggg caacttcaag 600
 gatgcccttg agttgtggg tgccgttatt ttgttgaggt tcgaacccga gctgctgatc 660
 cttaccatcc tggtcttcac gatcaagtcc ttctgggtt cctccgacaa caagaacaag 720
 gtcattaagg ccatcaacaa cgcctgaag gagcgtgacg agaagtggaa ggaagtctat 780
 tccttcatcg tctcgaactg gatgaccaag atcaacaccc agttcaacaa gcgaaaggag 840
 cagatgttacc aggctctgca gaaccagggtc aacgccccatca agaccatcat cgagtccaaag 900
 tacaactcct acaccctgga ggagaagaac gagcttacca acaagtacga tatcaaggcag 960
 atcgagaacg agctgaacca gaaggcttcc atcgccatga acaacatcga caggttcctg 1020
 accgagtcct ccatctccta cctgtatgaag ctcatcaacg aggtcaagat caacaagctg 1080
 cgagagtacg acgagaatgt caagacgtac ctgctgaact acatcatcca gcacggatcc 1140
 atccgtaa 1149

<210> 28
<211> 382
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTe Hn

<400> 28
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
1 5 10 15
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
20 25 30
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
35 40 45
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
50 55 60
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
65 70 75 80
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
85 90 95
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
100 105 110
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
115 120 125
Ile Tyr Thr Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
130 135 140
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145 150 155 160
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
165 170 175
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
180 185 190
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
195 200 205
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
210 215 220
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
225 230 235 240
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
245 250 255
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
260 265 270
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
275 280 285
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
290 295 300
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
305 310 315 320
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile
325 330 335
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
340 345 350
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
355 360 365
Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu

370

375

380

<210> 29
<211> 1227
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTF Hn

<400> 29
atggcccac cacgtctgtg tattagagtc aacaactcag aattattctt tgcgttcc 60
gagtcaagct acaacgagaa cgatattaac acacctaag agattgacga tactaccaac 120
ctaaacaaca actaccggaa caacttggat gaggttattt tggattacaa ctcacagacc 180
atccctcaaa tttccaaccc taccttaaac actcttgtcc aagacaactc ctacgttcca 240
agatacgatt ctaacggtac ctcagagatc gaggagtatg atgttgttga cttaacgtc 300
tttttctatt tgcatttgcga gaaggtgcca gaaggtgaaa ccaacatctc attgacttct 360
tccatttgata ccgccttgcgtt ggaagagtc aaggatatct tctttcttc ggagtttac 420
gatactatca acaagcctgt caacgcccgt ctgttcatcg attggattag caaggtcatc 480
agagatttta ccactgaagc tactcaaaa tccactgttgcata agatcttc 540
ttgattgtcc cctatgtcgg tcttgcatttgcata aacatcatttgcata ttgaggcaga aaaggtaac 600
tttgaggagg cttttgcatttgcata gttggggatgttgcata ttgaggatgttgcata tccagaactt 660
accatttcgt tcattttgttgcata aagtcttgcata tcgattcata cgagaacaag 720
aataaagcaa tttaaagctat taacaactcc ttgatcgaaa gagaggctaa gtggaaaggaa 780
atctactcat ggattgtatc aaactggctt actagaatttgcata acactcaatttgcata taacaagaga 840
aaggagcaaa tgcgttgcata aacttgcata aacttgcata tgcgttgcata tgcgttgcata 900
tacaagtaca acaactatac ttccgtatgttgcata aagaacagac ttgatctgcata atacaatatac 960
aacaacatttgcata aagaagagtttgcata gaacaagaaa gtttcttgcata ctatgttgcata tgcgttgcata 1020
tttatgttgcata aatccttgcata ctcttgcata atgttgcata tcaatgttgcata tgcgttgcata 1080
aaggatgttgcata agtacgatataa ccacgttgcata agcgttgcata tgcgttgcata tgcgttgcata 1140
agatcaatcc ttggagagca gacaaacgag ctgttgcata ttggatgttgcata cacttgcata 1200
tcctccatttgcata catttgcata ttcttgcata 1227

<210> 30
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTF Hn

<400> 30
Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
1 5 10 15
Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
20 25 30
Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
35 40 45
Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
50 55 60
Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
65 70 75 80
Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
85 90 95
Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly

100	105	110													
Glu	Thr	Asn	Ile	Ser	Leu	Thr	Ser	Ser	Ile	Asp	Thr	Ala	Leu	Leu	Glu
115						120				125					
Glu	Ser	Lys	Asp	Ile	Phe	Phe	Ser	Ser	Glu	Phe	Ile	Asp	Thr	Ile	Asn
130						135					140				
Lys	Pro	Val	Asn	Ala	Ala	Leu	Phe	Ile	Asp	Trp	Ile	Ser	Lys	Val	Ile
145						150				155				160	
Arg	Asp	Phe	Thr	Thr	Glu	Ala	Thr	Gln	Lys	Ser	Thr	Val	Asp	Lys	Ile
						165			170				175		
Ala	Asp	Ile	Ser	Leu	Ile	Val	Pro	Tyr	Val	Gly	Leu	Ala	Leu	Asn	Ile
						180			185				190		
Ile	Ile	Glu	Ala	Glu	Lys	Gly	Asn	Phe	Glu	Glu	Ala	Phe	Glu	Leu	Leu
						195			200				205		
Gly	Val	Gly	Ile	Leu	Leu	Glu	Phe	Val	Pro	Glu	Leu	Thr	Ile	Pro	Val
						210			215				220		
Ile	Leu	Val	Phe	Thr	Ile	Lys	Ser	Tyr	Ile	Asp	Ser	Tyr	Glu	Asn	Lys
225						230				235				240	
Asn	Lys	Ala	Ile	Lys	Ala	Ile	Asn	Asn	Ser	Leu	Ile	Glu	Arg	Glu	Ala
						245			250				255		
Lys	Trp	Lys	Glu	Ile	Tyr	Ser	Trp	Ile	Val	Ser	Asn	Trp	Leu	Thr	Arg
						260			265				270		
Ile	Asn	Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu	Gln	Met	Tyr	Gln	Ala	Leu
						275			280				285		
Gln	Asn	Gln	Val	Asp	Ala	Ile	Lys	Thr	Ala	Ile	Glu	Tyr	Lys	Tyr	Asn
						290			295				300		
Asn	Tyr	Thr	Ser	Asp	Glu	Lys	Asn	Arg	Leu	Glu	Ser	Glu	Tyr	Asn	Ile
						305			310				315		320
Asn	Asn	Ile	Glu	Glu	Glu	Leu	Asn	Lys	Lys	Val	Ser	Leu	Ala	Met	Lys
						325			330				335		
Asn	Ile	Glu	Arg	Phe	Met	Thr	Glu	Ser	Ser	Ile	Ser	Tyr	Leu	Met	Lys
						340			345				350		
Leu	Ile	Asn	Glu	Ala	Lys	Val	Gly	Lys	Leu	Lys	Lys	Tyr	Asp	Asn	His
						355			360				365		
Val	Lys	Ser	Asp	Leu	Leu	Asn	Tyr	Ile	Leu	Asp	His	Arg	Ser	Ile	Leu
						370			375				380		
Gly	Glu	Gln	Thr	Asn	Glu	Leu	Ser	Asp	Leu	Val	Thr	Ser	Thr	Leu	Asn
						385			390				395		400
Ser	Ser	Ile	Pro	Phe	Glu	Leu	Ser								
						405									

<210> 31
<211> 1233
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTG Hn

<400> 31
atggccaaaa ataccgtaa atctgaacag tgtattattg ttaataatga ggatttattt 60
ttcatagcta ataaagatag ttttcaaaa gattagctt aagcagaaac tatagcataat 120
aatacacaaa ataatactat agaaaataat ttttctatag atcagtttat ttttagataat 180
gattnaagca gtggcataga ctaccaaat gaaaacacag aaccattttac aaattttgac 240
gacatagata tccctgtgtt tattaaacaa tctgcttaa aaaaaatttt tttggatgg 300
gatagccttt ttgaatattt acatgctcaa acatttcctt ctaatataaa aaatctacaa 360
ctaacgaatt cattaaatga tgccttaaga aataataata aagtctatac ttttttttct 420

acaaaccttg ttgaaaaagc taatacagtt gtaggtgctt cacttttgt aaactggta 480
aaaggagtaa tagatgatt tacatctgaa tccacacaaa aaagtactat agataaaagtt 540
tcagatgtat ccataattat tccctatata ggacctgctt tgaatgtagg aaatgaaaca 600
gctaaagaaa attttaaaaa tgctttgaa ataggtggag ccgctatctt aatggagttt 660
attccagaac ttattgtacc tatagttgaa tttttacat tagaatcata tgttaggaaat 720
aaagggcata ttattatgac gatatccaaat gctttaaaga aaagggatca aaaatggaca 780
gatatgtatg gtttgatagt atcgcagtgg ctctcaacgg ttaatactca attttataca 840
ataaaagaaa gaatgtacaa tgctttaaat aatcaatcac aagcaataga aaaaataata 900
gaagatcaat ataatagata tagtgaagaa gataaaatga atattaacat tgatttaat 960
gatatagatt ttaaacttaa tcaaagtata aatttagcaa taaacaatat agatgatttt 1020
ataaaccaat gttctatatc atatctaatg aatagaatga ttccatttagc tgtaaaaaag 1080
ttaaaagact ttgatgataa tcttaagaga gatttattgg agtataataga tacaaatgaa 1140
ctatattac ttgatgaagt aaatattcta aaatcaaaag taaatagaca cctaaaagac 1200
agtataccat ttgatcttc actatatacc taa 1233

<210> 32
<211> 410
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTG Hn

<400> 32
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
1 5 10 15
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
20 25 30
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
35 40 45
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
50 55 60
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
65 70 75 80
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
85 90 95
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
100 105 110
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
115 120 125
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
130 135 140
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
145 150 155 160
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
165 170 175
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro
180 185 190
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala
195 200 205
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu
210 215 220
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn
225 230 235 240
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp
245 250 255

Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser
 260 265 270
 Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala
 275 280 285
 Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr
 290 295 300
 Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn
 305 310 315 320
 Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn
 325 330 335
 Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg
 340 345 350
 Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu
 355 360 365
 Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu
 370 375 380
 Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp
 385 390 395 400
 Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr
 405 410

<210> 33
 <211> 1314
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTF Hc

<400> 33
 gaattcacga tgtcttacac taacgacaaa atcctgatcc tgtacttcaa caaactgtac 60
 aaaaaaatca aagacaactc tattcctggac atgcgttacg aaaacaacaa attcatcgac 120
 atctctggct atggttctaa catctctatc aacgggtgacg tctacatcta ctctacta 180
 cgcaaccagt tcggtatcta ctcttctaaa ccgtctgaag taaacatcgc tcagaacaac 240
 gacatcatct acaacggtcg ttaccagaac ttctcttatct ctttctgggt tcgtatcccg 300
 aaatacttca acaaaggtaa cctgaacaac gaatacacta tcatcgactg catccgtAAC 360
 aacaactctg gttggaaaat ctctctgaac tacaacaaaa tcatctggac tctgcaggac 420
 actgctggta acaaccagaa actggttttc aactacactc agatgatctc tatctctgac 480
 tacattaata aatggatctt cgttactatc actaacaacc gtctgggtaa ctctcgtatc 540
 tacatcaacg gtaacctgat cgatggaaaaa tctatctcta acctgggtga catccacgtt 600
 tctgacaaca tcctgttcaa aatcggttgg tgcaacgaca cgcgttacgt tggtatccgt 660
 tacttcaaag ttttcgacac tgaactgggt aaaactgaaa tcgaaactct gtactctgac 720
 gaaccggacc cgtctatcct gaaagacttc tggggtaact acctgctgtca caacaaacgt 780
 tactacctgc tgaacctgct ccggactgac aaatctatca ctcagaactc taacttcctg 840
 aacatcaacc agcagcgtgg tggttatcag aaacctaata tcttctctaa cactcgatcg 900
 tacactgggt ttgaaggatcatccgtaaa aacgggttcta ctgacatctc taacactgac 960
 aacttcgtac gtaaaaacga cctggcttac atcaacgttgg ttgaccgttca cggttac 1020
 cgtctgtacg ctgacatctc tattcgctaaa ccggaaaaaaa tcataactt gatccgtact 1080
 tctaaactcta acaactctt gggtcagatc atcggtatgg actcgatcg taacaactgc 1140
 actatgaact tccagaacaa caacgggtt aacatcgatcg tgctgggtt ccactcta 1200
 aacctgggtt cttcttcatg gtactacaac aacatccgtaa aaaacacttc ttcttaacgg 1260
 tgcttctgtt ctttcatctc taaaagaacac gggttggcagg aaaactaaga attc 1314

<210> 34
 <211> 432
 <212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTF Hc

<400> 34

Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
1 5 10 15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
20 25 30
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
35 40 45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
50 55 60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
65 70 75 80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
85 90 95
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
100 105 110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
115 120 125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
130 135 140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
145 150 155 160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
165 170 175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
180 185 190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
195 200 205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
210 215 220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
225 230 235 240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
245 250 255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
260 265 270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
275 280 285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
290 295 300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
305 310 315 320
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
325 330 335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
340 345 350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
355 360 365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
370 375 380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
385 390 395 400

Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
405 410 415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
420 425 430

<210> 35
<211> 1278
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTe Hc

<400> 35
ttcgaaaacga tgatttaat ttccctacttc aacaagttct tcaagagaat taagtcttct 60
tccgtttaa acatgagata caagaatgat aaatacgtcg acacttccgg ttacgactcc 120
aatatcaaca ttaacggta cgtgtacaag taccctaacta acaaaaacca attcggtatc 180
tacaacgaca agcttactga gctgaacatc tctcaaaacg actacattat ctacgacaac 240
aagtacaata acttctctat ttctttctgg gtcagaattc ctaactacga taacaagatc 300
gtcaacgtta acaacgagta cactatcatc aactgtatga gagacaacaa ctccgggttgg 360
aaggtctctc ttaaccacaa cgagatgatt tggaccttgc aagacaacgc aggtattaac 420
caaaaagttag cattcaacta cgtaaacgca aacggattt ctgactacat caacaagtgg 480
atttcgtca ctatcactaa cgacagatta ggggactcta agctttacat taacggtaac 540
ttaatcgacc aaaagtccat tttaaactta ggtAACATTc acgtttctga caacatctta 600
ttcaagatcg ttaactgcag ttacaacaga tacattggca ttagatactt caacattttc 660
gacaaggagt tagacgagac cgagattcaa actttataca gcaacgaacc taacaccaat 720
attttgaagg acttctgggg taactacttg cttaacgaca aggaataacta cttattaaac 780
gtgttaaagc caaacaactt cattgatagg agaaaggatt ctactttaag cattaacaac 840
atcagaagca ctattcttt agctaacaga ttataactctg gtatcaaggt taagatccaa 900
agagttaca actcttctac taacgataac cttgttagaa agaacgatca ggtctatatt 960
aacttcgtcg ctagcaagac tcacttatttc ccattatatg ctgataacgc taccaccaac 1020
aaggagaaga ccatcaagat ctccctcctct ggcaacagat ttaaccaagt cgtcggtatg 1080
aactccgtcg gtaacaactg taccatgaac tttaaaaata ataatggaaa taatattggg 1140
tgtttaggtt tcaaggcaga tactgttagt gctgtactt ggtattatac ccacatgaga 1200
gatcacacca acagcaatgg atgttttgg aactttattt ctgaagaaca tggatggcaa 1260
gaaaaataat agggatcc 1278

<210> 36
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTe Hc

<400> 36
Met Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
1 5 10 15
Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr
20 25 30
Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr
35 40 45
Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu
50 55 60
Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys

65	70	75	80
Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys			
85	90	95	
Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp			
100	105	110	
Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp			
115	120	125	
Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr			
130	135	140	
Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val			
145	150	155	160
Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly			
165	170	175	
Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val			
180	185	190	
Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr			
195	200	205	
Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr			
210	215	220	
Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys			
225	230	235	240
Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu			
245	250	255	
Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr			
260	265	270	
Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu			
275	280	285	
Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr			
290	295	300	
Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val			
305	310	315	320
Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr			
325	330	335	
Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn			
340	345	350	
Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe			
355	360	365	
Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp			
370	375	380	
Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr			
385	390	395	400
Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp			
405	410	415	
Gln Glu Lys			

<210> 37
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTA Hc

<400> 37
ctcgagccat ggctcgctcg ctgtctacct tcactgaata catcaagaac atcatcaata 60

cctccatcct gaacctgcgc tacgaatcca atcacctgat cgacctgtct cgctacgctt 120
 cccaaatcaa catcggttct aaagttaact tcgatccgat cgacaagaat cagatccagc 180
 tggtaatctt ggaatcttcc aaaatcgaag ttatcctgaa gaatgctatc gtatacaact 240
 ctatgtacga aaacttctcc acctccttct ggatccgtat cccgaaataac ttcaactcca 300
 tctctctgaa caatgaatac accatcatca actgcatgga aaacaattct gggtggaaag 360
 tatctctgaa ctacggtaatc atcatctgga ctctgcagga cactcagggaa atcaaacagc 420
 gtgttgtatt caaatactct cagatgatca acatctctga ctacatcaat cgctggatct 480
 tcggttaccat caccacaat cgtctgaata actccaaaat ctacatcaac ggcggctctga 540
 tcgaccagaa accgatctcc aatctggta acatccacgc ttctaaataac atcatgttca 600
 aactggacgg ttgtcgac actcaccgct acatctggat caaatacttc aatctgttgc 660
 acaaagaact gaacgaaaaa gaaatcaaag acctgtacga caaccagttcc aattctggta 720
 tcctgaaaga cttctgggt gactacctgc agtacgacaa accgtactac atgctgaatc 780
 tgtacgatcc gaacaatac gttgacgtca acaatgttgcgatc tacatgttacc 840
 tgaaaaggcttcc gctgtgttct gtatgacta ccaacatcta cctgaactct tccctgttacc 900
 gtggtaacaa attcatcatc aagaaaatacg cgtctgttac caaggacaat atcgttgc 960
 acaatgatcg tgtatacatc aatgttgcgatc ttaagaacaa agaataccgt ctggctacca 1020
 atgcttctca ggctgggtta gaaaagatct tgcgtcttgcgatc gacgttggta 1080
 atctgtctca ggttagttgtta atgaaatcca agaacgacca gggtatcact aacaaatgca 1140
 aaatgaatct gcaggacaac aatggtaacg atatcggtt catcggttcc caccagttca 1200
 acaatatcgc taaactgggtt gcttccaact ggtacaatcg tcagatcgaa cgttcctctc 1260
 gcactctggg ttgctttgg gagttcatcc cggttgcgatc cggttgggtt gaacgtccgc 1320
 tgtaacccgg gaaagctt 1338

<210> 38
 <211> 415
 <212> PRT
 <213> Clostridium botulinum

<400> 38
 Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys
 1 5 10 15
 Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln
 20 25 30
 Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys
 35 40 45
 Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
 50 55 60
 Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu
 65 70 75 80
 Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser
 85 90 95
 Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile
 100 105 110
 Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp
 115 120 125
 Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn
 130 135 140
 Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile
 145 150 155 160
 Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu
 165 170 175
 Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Phe Tyr Phe Asn
 180 185 190
 Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp
 195 200 205
 Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu
 210 215 220

Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys
 225 230 235 240
 Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys
 245 250 255
 Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser
 260 265 270
 Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn
 275 280 285
 Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val
 290 295 300
 Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly
 305 310 315 320
 Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu
 325 330 335
 Ser Gln Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn
 340 345 350
 Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe
 355 360 365
 Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn
 370 375 380
 Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser
 385 390 395 400
 Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
 405 410 415

<210> 39
 <211> 1351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTB Hc

<400> 39
 atggcttca acaaatacaa ttccgaaaatc ctgaaacaata tcatcctgaa cctgcgttac 60
 aaagacaaca atctgatcga tctgtctgg tacgggtcta aagttgaagt atacgacgg 120
 gttgaactga atgacaagaa ccagttcaaa ctgacctctt ccgctaaactc taagatccgt 180
 gttactcaga atcagaacat catcttcaac tccgttattcc tggacttctc tgtttccttc 240
 tggatccgta tcccggaaata caagaacgac ggtatccaga attacatcca caatgaatac 300
 accatcatca actgcatgaa gaataactct ggttggaaaga tctccatccg cggtaaccgt 360
 atcatctgga ctctgatcga tatcaacggt aagaccaaatt ctgttattctt cgaataacaac 420
 atccgtgaag acatctctga atacatcaat cgctggttct tcgttaccat cacaataaac 480
 ctgaacaatg ctaaaatcta catcaacggt aaactggaaat ctaataccga catcaaagac 540
 atccgtgaag ttatcgctaa cgggtggaaatc atcttcaaacc tggacgggtga catcgatcgt 600
 acccagttca tctggatgaa atacttctcc atcttcaaca cccgaaactgtc tcagtc 660
 atcgaagaac ggtacaagat ccagtcttac tccgaatacc tggaaagactt ctggggtaat 720
 ccgctgatgt acaacaaaaga atactatatg ttcaatgctg gtaacaagaa ctcttacatc 780
 aaactgaaga aagactctcc ggttgggtaa atccgtactc gttccaaata caaccagaac 840
 tctaaatatac tcaactaccg cggactgtac atccgtgaaa agttcatcat cggtcgcaaa 900
 tctaaactctc agtccatcaa tggatgacatc gtacgtaaag aagactcatc ctacctggac 960
 ttcttcaacc tgaatcagga atggcgtgtac tacacccata agtacttcaa gaaagaagaa 1020
 gaaaagcttt tcctggctcc gatctctgtat tccgacgaaac tctacaacac catccagatc 1080
 aaagaataacg acgaacagcc gacctactct tgccagctgc tggtaagaa agatgaagaa 1140
 tctactgacg aaatcggtct gatcggtatc caccgttct acgaatctgg tatcgatattc 1200
 gaagaataaca aagactactt ctgcatactcc aaatggtacc tgaaggaagt taaacgcaaa 1260
 ccgtacaacc tgaaaactggg ttgcaattgg cagttcatcc cgaaagacga aggttggacc 1320

<210> 40
<211> 439

<212> PRT
<213> Clostridium botulinum

<400> 40
Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn Leu
1 5 10 15
Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala Lys
20 25 30
Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe Lys
35 40 45
Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln Asn
50 55 60
Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp Ile
65 70 75 80
Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His Asn
85 90 95
Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys Ile
100 105 110
Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn Gly
115 120 125
Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile Ser
130 135 140
Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu Asn
145 150 155 160
Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp Ile
165 170 175
Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys Leu
180 185 190
Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe Ser
195 200 205
Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr Lys
210 215 220
Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro Leu
225 230 235 240
Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser
245 250 255
Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr Arg
260 265 270
Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu Tyr
275 280 285
Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile
290 295 300
Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe Phe
305 310 315 320
Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys Lys
325 330 335
Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu Phe
340 345 350
Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr Ser
355 360 365
Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile Gly
370 375 380
Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu Glu

385	390	395	400
Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys			
405	410	415	
Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro			
420	425	430	
Lys Asp Glu Gly Trp Thr Glu			
435			

<210> 41
 <211> 848
 <212> PRT
 <213> Clostridium botulinum

<400> 41			
Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe			
1	5	10	15
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu			
20	25	30	
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu			
35	40	45	
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro			
50	55	60	
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu			
65	70	75	80
Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu			
85	90	95	
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu			
100	105	110	
His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu			
115	120	125	
Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys			
130	135	140	
Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu			
145	150	155	160
Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr			
165	170	175	
Asp Lys Ile Ala Asp Ile Thr Ile Ile Pro Tyr Ile Gly Pro Ala			
180	185	190	
Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu			
195	200	205	
Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala			
210	215	220	
Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys			
225	230	235	240
Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu			
245	250	255	
Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys			
260	265	270	
Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu			
275	280	285	
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn			
290	295	300	
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp			
305	310	315	320
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile			
325	330	335	

Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met
340 345 350
Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys
355 360 365
Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly
370 375 380
Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp
385 390 395 400
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser
405 410 415
Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn
420 425 430
Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser
435 440 445
Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn
450 455 460
Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu
465 470 475 480
Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser
485 490 495
Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn
500 505 510
Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val
515 520 525
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu
530 535 540
Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser
545 550 555 560
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu
565 570 575
Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro
580 585 590
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys
595 600 605
Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe
610 615 620
Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr
625 630 635 640
Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr
645 650 655
Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn
660 665 670
Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu
675 680 685
Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser
690 695 700
Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly
705 710 715 720
Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val
725 730 735
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala
740 745 750
Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
755 760 765
Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
770 775 780
Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly

785	790	795	800
Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser			
805	810	815	
Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys			
820	825	830	
Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu			
835	840	845	

<210> 42
 <211> 850
 <212> PRT
 <213> Clostridium botulinum

<400> 42			
Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe Ile			
1	5	10	15
Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg Ile			
20	25	30	
Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile Asn			
35	40	45	
Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro Ser			
50	55	60	
Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val Tyr			
65	70	75	80
Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr Ile			
85	90	95	
Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp Ile			
100	105	110	
Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys Val			
115	120	125	
Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val Val			
130	135	140	
Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp Phe			
145	150	155	160
Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp Ile			
165	170	175	
Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn Glu			
180	185	190	
Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala Ser			
195	200	205	
Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly Ala			
210	215	220	
Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys Thr			
225	230	235	240
Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met Tyr			
245	250	255	
Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe Tyr			
260	265	270	
Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln Ala			
275	280	285	
Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys Glu			
290	295	300	
Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu Asn			
305	310	315	320
Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn Gly			
325	330	335	

Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val Glu
340 345 350
Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn Tyr
355 360 365
Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu Lys
370 375 380
Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu Ser
385 390 395 400
Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe Asn Lys Tyr Asn
405 410 415
Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn Leu Arg Tyr Lys Asp Asn
420 425 430
Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala Lys Val Glu Val Tyr Asp
435 440 445
Gly Val Glu Leu Asn Asp Lys Asn Gln Phe Lys Leu Thr Ser Ser Ala
450 455 460
Asn Ser Lys Ile Arg Val Thr Gln Asn Gln Asn Ile Ile Phe Asn Ser
465 470 475 480
Val Phe Leu Asp Phe Ser Val Ser Phe Trp Ile Arg Ile Pro Lys Tyr
485 490 495
Lys Asn Asp Gly Ile Gln Asn Tyr Ile His Asn Glu Tyr Thr Ile Ile
500 505 510
Asn Cys Met Lys Asn Asn Ser Gly Trp Lys Ile Ser Ile Arg Gly Asn
515 520 525
Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn Gly Lys Thr Lys Ser Val
530 535 540
Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile Ser Glu Tyr Ile Asn Arg
545 550 555 560
Trp Phe Phe Val Thr Ile Thr Asn Asn Leu Asn Asn Ala Lys Ile Tyr
565 570 575
Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp Ile Lys Asp Ile Arg Glu
580 585 590
Val Ile Ala Asn Gly Glu Ile Ile Phe Lys Leu Asp Gly Asp Ile Asp
595 600 605
Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe Ser Ile Phe Asn Thr Glu
610 615 620
Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr Lys Ile Gln Ser Tyr Ser
625 630 635 640
Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro Leu Met Tyr Asn Lys Glu
645 650 655
Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr Ile Lys Leu Lys
660 665 670
Lys Asp Ser Pro Val Gly Glu Ile Leu Thr Arg Ser Lys Tyr Asn Gln
675 680 685
Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu Tyr Ile Gly Glu Lys Phe
690 695 700
Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile Asn Asp Asp Ile Val
705 710 715 720
Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe Phe Asn Leu Asn Gln Glu
725 730 735
Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys Lys Glu Glu Lys Leu
740 745 750
Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu Phe Tyr Asn Thr Ile Gln
755 760 765
Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr Ser Cys Gln Leu Leu Phe
770 775 780
Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile Gly Leu Ile Gly Ile His

785	790	795	800
Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu Glu Tyr Lys Asp Tyr Phe			
805	810	815	
Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro Tyr Asn			
820	825	830	
Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro Lys Asp Glu Gly Trp			
835	840	845	
Thr Glu			
850			

<210> 43
 <211> 1296
 <212> PRT
 <213> Clostridium botulinum

<300>
 <308> X52066
 <309> 1993-04-23

<400> 43			
Met Gln Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly			
1	5	10	15
Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Val Gly Gln Met Gln Pro			
20	25	30	
Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg			
35	40	45	
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu			
50	55	60	
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr			
65	70	75	80
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu			
85	90	95	
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val			
100	105	110	
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys			
115	120	125	
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr			
130	135	140	
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile			
145	150	155	160
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr			
165	170	175	
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe			
180	185	190	
Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu			
195	200	205	
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu			
210	215	220	
Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn			
225	230	235	240
Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu			
245	250	255	
Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys			
260	265	270	
Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn			
275	280	285	

Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
290 295 300
Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305 310 315 320
Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
325 330 335
Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
340 345 350
Asn Phe Val Lys Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
355 360 365
Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
370 375 380
Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385 390 395 400
Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
405 410 415
Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
420 425 430
Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys
435 440 445
Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
450 455 460
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
465 470 475 480
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
485 490 495
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
500 505 510
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
515 520 525
Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
530 535 540
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
545 550 555 560
His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
565 570 575
Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
580 585 590
Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
595 600 605
Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
610 615 620
Asp Lys Ile Ala Asp Ile Thr Ile Ile Pro Tyr Ile Gly Pro Ala
625 630 635 640
Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
645 650 655
Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
660 665 670
Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
675 680 685
Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
690 695 700
Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
705 710 715 720
Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
725 730 735
Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn

740	745	750
Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp		
755	760	765
Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile		
770	775	780
Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met		
785	790	795
Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys		
805	810	815
Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly		
820	825	830
Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp		
835	840	845
Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser		
850	855	860
Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn		
865	870	875
Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser		
885	890	895
Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn		
900	905	910
Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu		
915	920	925
Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser		
930	935	940
Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn		
945	950	955
Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val		
965	970	975
Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu		
980	985	990
Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser		
995	1000	1005
Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu		
1010	1015	1020
Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro		
1025	1030	1035
Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys		
1045	1050	1055
Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe		
1060	1065	1070
Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr		
1075	1080	1085
Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr		
1090	1095	1100
Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn		
1105	1110	1115
Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu		
1125	1130	1135
Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser		
1140	1145	1150
Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly		
1155	1160	1165
Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val		
1170	1175	1180
Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala		
1185	1190	1195
		1200

Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
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 Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
 1220 1225 1230
 Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
 1235 1240 1245
 Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser
 1250 1255 1260
 Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys
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 Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu
 35 40 45
 Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly
 50 55 60
 Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn
 65 70 75 80
 Thr Asn Asp Lys Lys Asn Ile Phe Leu Gln Thr Met Ile Lys Leu Phe
 85 90 95
 Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile
 100 105 110
 Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu
 115 120 125
 Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn
 130 135 140
 Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile
 145 150 155 160
 Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly
 165 170 175
 Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln
 180 185 190
 Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu
 195 200 205
 Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro
 210 215 220
 Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr
 225 230 235 240
 Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe
 245 250 255
 Phe Met Gln Ser Thr Asp Ala Ile Gln Ala Glu Glu Leu Tyr Thr Phe

260	265	270
Gly Gly Gln Asp Pro Ser Ile Ile Thr Pro Ser Thr Asp Lys Ser Ile		
275	280	285
Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val Asp Arg Leu Asn		
290	295	300
Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr		
305	310	315
Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu Asp Ser Glu Gly		
325	330	335
Lys Tyr Ser Ile Asp Val Glu Ser Phe Asp Lys Leu Tyr Lys Ser Leu		
340	345	350
Met Phe Gly Phe Thr Glu Thr Asn Ile Ala Glu Asn Tyr Lys Ile Lys		
355	360	365
Thr Arg Ala Ser Tyr Phe Ser Asp Ser Leu Pro Pro Val Lys Ile Lys		
370	375	380
Asn Leu Leu Asp Asn Glu Ile Tyr Thr Ile Glu Glu Gly Phe Asn Ile		
385	390	395
Ser Asp Lys Asp Met Glu Lys Glu Tyr Arg Gly Gln Asn Lys Ala Ile		
405	410	415
Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His Leu Ala Val Tyr		
420	425	430
Lys Ile Gln Met Cys Lys Ser Val Lys Ala Pro Gly Ile Cys Ile Asp		
435	440	445
Val Asp Asn Glu Asp Leu Phe Phe Ile Ala Asp Lys Asn Ser Phe Ser		
450	455	460
Asp Asp Leu Ser Lys Asn Glu Arg Ile Glu Tyr Asn Thr Gln Ser Asn		
465	470	475
Tyr Ile Glu Asn Asp Phe Pro Ile Asn Glu Leu Ile Leu Asp Thr Asp		
485	490	495
Leu Ile Ser Lys Ile Glu Leu Pro Ser Glu Asn Thr Glu Ser Leu Thr		
500	505	510
Asp Phe Asn Val Asp Val Pro Val Tyr Glu Lys Gln Pro Ala Ile Lys		
515	520	525
Lys Ile Phe Thr Asp Glu Asn Thr Ile Phe Gln Tyr Leu Tyr Ser Gln		
530	535	540
Thr Phe Pro Leu Asp Ile Arg Asp Ile Ser Leu Thr Ser Ser Phe Asp		
545	550	555
Asp Ala Leu Leu Phe Ser Asn Lys Val Tyr Ser Phe Phe Ser Met Asp		
565	570	575
Tyr Ile Lys Thr Ala Asn Lys Val Val Glu Ala Gly Leu Phe Ala Gly		
580	585	590
Trp Val Lys Gln Ile Val Asn Asp Phe Val Ile Glu Ala Asn Lys Ser		
595	600	605
Asn Thr Met Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Ile		
610	615	620
Gly Leu Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Gly Asn Phe Glu		
625	630	635
Asn Ala Phe Glu Ile Ala Gly Ala Ser Ile Leu Leu Glu Phe Ile Pro		
645	650	655
Glu Leu Leu Ile Pro Val Val Gly Ala Phe Leu Leu Glu Ser Tyr Ile		
660	665	670
Asp Asn Lys Asn Lys Ile Ile Lys Thr Ile Asp Asn Ala Leu Thr Lys		
675	680	685
Arg Asn Glu Lys Trp Ser Asp Met Tyr Gly Leu Ile Val Ala Gln Trp		
690	695	700
Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Gly Met Tyr		
705	710	715
		720

Lys Ala Leu Asn Tyr Gln Ala Gln Ala Leu Glu Glu Ile Ile Lys Tyr
725 730 735
Arg Tyr Asn Ile Tyr Ser Glu Lys Glu Lys Ser Asn Ile Asn Ile Asp
740 745 750
Phe Asn Asp Ile Asn Ser Lys Leu Asn Glu Gly Ile Asn Gln Ala Ile
755 760 765
Asp Asn Ile Asn Asn Phe Ile Asn Gly Cys Ser Val Ser Tyr Leu Met
770 775 780
Lys Lys Met Ile Pro Leu Ala Val Glu Lys Leu Leu Asp Phe Asp Asn
785 790 795 800
Thr Leu Lys Lys Asn Leu Leu Asn Tyr Ile Asp Glu Asn Lys Leu Tyr
805 810 815
Leu Ile Gly Ser Ala Glu Tyr Glu Lys Ser Lys Val Asn Lys Tyr Leu
820 825 830
Lys Thr Ile Met Pro Phe Asp Leu Ser Ile Tyr Thr Asn Asp Thr Ile
835 840 845
Leu Ile Glu Met Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile
850 855 860
Ile Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly
865 870 875 880
Tyr Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys
885 890 895
Asn Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr
900 905 910
Gln Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val
915 920 925
Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn
930 935 940
Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser
945 950 955 960
Gly Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile
965 970 975
Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg
980 985 990
Glu Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr
995 1000 1005
Asn Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser
1010 1015 1020
Asn Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile
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Ile Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met
1045 1050 1055
Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu
1060 1065 1070
Glu Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp
1075 1080 1085
Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly
1090 1095 1100
Asn Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu
1105 1110 1115 1120
Ile Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr
1125 1130 1135
Arg Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn
1140 1145 1150
Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr
1155 1160 1165
Leu Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys

1170	1175	1180
Tyr Phe Lys Lys Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp		
1185	1190	1195
Ser Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln		1200
1205	1210	1215
Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr		
1220	1225	1230
Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile		
1235	1240	1245
Val Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu		
1250	1255	1260
Lys Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp		
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Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu		1280
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